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Translated Protein-Frames: 3-Nucleotide 111 to 1130
mz5004_vh.seq Length: 2691 24/Aug/1999

1 GCGGCCGCGTGACCATCACGTGCTCCAGCTACCAGGGCTACCCCTG
46 AGGCTGAGGTGTTCTGGCAGGATGGGCAGGGTGTGCCCTGACTG

91 GCAACGTGACCACGTGCGCAGATGGCCAACGAGCAGGGCTTGTTTG
MetAlaAsnGluGlnGlyLeuPheA

136 ATGTGCACAGCATCCTGCGGGTGGTGCTGGGTGCAAATGGCACCT
spValHisSerIleLeuArgValValLeuGlyAlaAsnGlyThrT

181 ACAGCTGCCTGGTGCGCAACCCCGTGCTGCAGCAGGATGCGCACA
yrSerCysLeuValArgAsnProValLeuGlnGlnAspAlaHisS

226 GCTCTGTCACCATCACACCCAGAGAAGCCCCACAGGAGCCGTGG
erSerValThrIleThrProGlnArgSerProThrGlyAlaValG

271 AGGTCCAGGTCCCTGAGGACCCGGTGGTGGCCCTAGTGGGCACCG
luValGlnValProGluAspProValValAlaLeuValGlyThrA

316 ATGCCACCCTGCACCTGCTCCTTCTCCCCGAGCCTGGCTTCAGCC
spAlaThrLeuHisCysSerPheSerProGluProGlyPheSerL

361 TGACACAGCTCAACCTCATCTGGCAGCTGACAGACACCAAACAGC
euThrGlnLeuAsnLeuIleTrpGlnLeuThrAspThrLysGlnL

406 TGGTGCACAGTTTTCACCGAAGGCCGGGACCAGGGCAGCGCTATG
euValHisSerPheThrGluGlyArgAspGlnGlySerAlaTyrA

451 CCAACCGCACGGCCCTCTTCCCGGACCTGCTGGCACAAGGCAATG
laAsnArgThrAlaLeuPheProAspLeuLeuAlaGlnGlyAsnA

496 CATCCCTGAGGCTGCAGCGCGTGCGTGTGGCGGACGAGGGCAGCT
laSerLeuArgLeuGlnArgValArgValAlaAspGluGlySerP

541 TCACCTGCTTCGTGAGCATCCGGGATTTCCGGCAGCGCTGCCGTCA
heThrCysPheValSerIleArgAspPheGlySerAlaAlaValS

586 GCCTGCAGGTGGCCGCTCCCTACTCGAAGCCCAGCATGACCCTGG
erLeuGlnValAlaAlaProTyrSerLysProSerMetThrLeuG

631 AGCCCAACAAGGACCTGCGGCCAGGGGACACGGTGACCATCACGT
luProAsnLysAspLeuArgProGlyAspThrValThrIleThrC

676 GCTCCAGCTACCGGGGCTACCCTGAGGCTGAGGTGTTCTGGCAGG
ysSerSerTyrArgGlyTyrProGluAlaGluValPheTrpGlnA

721 ATGGGCAGGGTGTGCCCTGACTGGCAACGTGACCACGTGCGAGA
spGlyGlnGlyValProLeuThrGlyAsnValThrThrSerGLnM

766 TGGCCAACGAGCAGGGCTTGTTTGATGTGCACAGCGTCTGCGGG
etAlaAsnGluGlnGlyLeuPheAspValHisSerValLeuArgV

Fig. 1

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811 TGGTGTCTGGGTGCGAATGGCACCTACAGCTGCCTGGTGGCGCAACC
alValLeuGlyAlaAsnGlyThrTyrSerCysLeuValArgAsnP

856 CCGTGTCTGCAGCAGGATGCGCACGGCTCTGTACCATCACAGGGC
roValLeuGlnGlnAspAlaHisGlySerValThrIleThrGlyG

901 AGCCTATGACATTCCCCCAGAGGCCCTGTGGGTGACCGTGGGGC
lnProMetThrPheProProGluAlaLeuTrpValThrValGlyL

946 TCTCTGTCTGTCTCATTGCACTGCTGGTGGCCCTGGCTTTCGTGT
euSerValCysLeuIleAlaLeuLeuValAlaLeuAlaPheValC

991 GCTGGAGAAAGATCAAACAGAGCTGTGAGGAGGAGAATGCAGGAG
ysTrpArgLysIleLysGlnSerCysGluGluGluAsnAlaGlyA

1036 CCGAGGACCAGGATGGGGAGGGAGAAGGCTCCAAGACAGCCCTGC
laGluAspGlnAspGlyGluGlyGluGlySerLysThrAlaLeuG

1081 AGCCTCTGAAACACTCTGACAGCAAAGAAGATGATGGACAAGAAA
lnProLeuLysHisSerAspSerLysGluAspAspGlyGlnGluI

1126 TAGCCTGACCATGAGGACCAGGGAGCTGCTACCCCTCCCTACAGC
leAla

1171 TCCTACCCCTCTGGCTGCAATGGGGCTGCACTGTGAGCCCTGCCCC
1216 CAACAGATGCATCTGTCTGACAGGTGGGCTCCTTCTCCAAAGG
1261 ATGCGATACACAGACCACTGTGCAGCCTTATTTCTCCAATGGACA
1306 TGATTTCCCAAGTCATCCTGTCTGCCTTTTTTCTTATAGACACAATG
1351 AACAGACCACCCACAACCTTAGTTCTCTAAGTCATCCTGCCTGCT
1396 GCCTTATTTTACAGTACATACATTTCTTAGGGACACAGTACACTG
1441 ACCACATCACCACCCTCTTCTTCCAGTGCTGCGTGGACCATCTGG
1486 CTGCCTTTTTTCTCCAAAGATGCAATATTCAGACTGACTGACCC
1531 CCTGCCTTATTTACCAAAGACACGATGCATAGTCACCCCGGCCT
1576 TGTTCCTCCAATGGCCGTGATACACTAGTGATCATGTTACGCCCT
1621 GCTTCCACCTGCATAGAATCTTTCTTCTCAGACAGGGACAGTGC
1666 GGCCTCAACATCTCCTGGAGTCTAGAAGCTGTTTCCTTTCCCCCTC
1711 CTTCCTCCTCTTGCTCTAGCCTTAATACTGGCCTTTTCCCTCCCT
1756 GCCCCAAGTGAAGACAGGGCACTCTGCGCCCAACACATGCACAGC
1801 TGTGCATGGAGACCTGCAGGTGCACGTGCTGGAACACGTGTGGTT
1846 CCCCCCTGGCCCAGCCTCCTCTGCAGTGCCCCCTCTCCCCTGCCCA
1891 TCCTCCCCACGGAAGCATGTGCTGGTCACACTGGTTCTCCAGGGG
1936 TCTGTGATGGGGCCCCCTGGGGGTGAGCTTCTGTCCCTCTGCCTTC
1981 TCACCTCTTTGTTCTTTCTTTTCATGTATCCATTAGTTGATGT
2026 TTATTGAGCAACTACAGATGTCAGCACTGTGTTAGGTGCTGGGGG
2071 CCCTGCGTGGGAAGATAAAGTTCCCTCCCTCAAGGACTCCCCATCC
2116 AGCTGGGAGACAGACAACCTAATACTGCACTGCACCCTGCGGTTTGCA
2161 GGGGGCTCCTGCCTGGCTCCCTGCTCCACACCTCCTCTGTGGCTC
2206 AAGGCTTCCTGGATACCTCACCCCCATCCCACCCATAATTCTTAC
2251 CCAGAGCATGGGGTTGGGGCGGAAACCTGGAGAGAGGGACATAGC
2296 CCCTCGCCACGGCTAGAGAATCTGGTGGTGTCAAAATGTCTGTC
2341 CAGGTGTGGGCAGGTGGGCAGGCACCAAGGCCCTCTGGACCTTTC
2386 ATAGCAGCAGAAAAGGCAGAGCCTGGGGCAGGGCAGGGCCAGGAA
2431 TGCTTTGGGGACACCGAGGGGACTGCCCCCACCCTTCCCTTGGG
2476 GCTATTCTGGGGCTGGGGCAGTCTTTTCTTGGCTTGCCCTTGCC
2521 AGCTCCCGGCCTCTGGTAGAGTGAGACTTCAGACGTTCTGATGCC

Fig. 1 Continued

2566 TTCCGGATGTCATCTCTCCCTGCCCCAGGAATGGAAGATGTGAGG
2611 ACTTCTAATTTAAATGTGGGACTCGGAGGGATTTTGTAAACTGGG
2656 GGTATATTTTGGGGAAAATAAATGTCTTTGTAAAA

Fig. 1 Continued

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Translated Protein-Frame: 2-Nucleotide 2 to 1324
Mz5004 12/16/99

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CCCTCTTCCCGGACCTGCTGGCACAGGGCAACGCATCCCTGAGGC
ProLeuProGlyProAlaGlyThrGlyGlnArgIleProGluAl
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TGCAGCGCGTGCCTGTAGCGGACGAGGGCAGCTTCACCTGCTTCG
aAlaAlaArgAlaCysSerGlyArgGlyGlnLeuHisLeuLeuAr
91
TGAGCATCCGGGATTTCCGGCAGCGCTGCCGTGAGCCTGCAGGTGG
gGluHisProGlyPheArgGlnArgCysArgGlnProAlaGlyG1
136
CCGCTCCCTACTCGAAGCCCAGCATGACCCTGGAGCCCAACAAGG
yArgSerLeuLeuGluAlaGlnHisAspProGlyAlaGlnGlnG1
181
ACCTGCGGCCAGGGGACACGGTGTGACCATCACGTGCTCCAGCTA
yProAlaAlaArgGlyHisGlyValThrIleThrCysSerSerTy
226
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rGlnGlyTyrProGluAlaGluValPheTrpGlnAspGlyGlnG1
271
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yValProLeuThrGlyAsnValThrThrSerGlnMetAlaAsnG1
316
GCAGGGCTTGTTTGATGTGCACAGCATCCTGCGGGTGGTGCTGGG
uGlnGlyLeuPheAspValHisSerIleLeuArgValValLeuG1
361
TGCAAATGGCACCTACAGCTGCCTGGTGCGCAACCCCGTGCTGCA
yAlaAsnGlyThrTyrSerCysLeuValArgAsnProValLeuG1
406
GCAGGATGCGCACAGCTCTGTCACCATCACACCCAGAGAAGCCC
nGlnAspAlaHisSerSerValThrIleThrProGlnArgSerPr
451
CACAGGAGCCGTGGAGGTCCAGGTCCCTGAGGACCCGGTGGTGGC
oThrGlyAlaValGluValGlnValProGluAspProValValAl
496
CCTAGTGGGCACCGATGCCACCCTGCACTGCTCCTTCTCCCCGA
aLeuValGlyThrAspAlaThrLeuHisCysSerPheSerProG1
541
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586
AGACACCAAACAGCTGGTGCACAGTTTCACCGAAGGCCGGGACCA
rAspThrLysGlnLeuValHisSerPheThrGluGlyArgAspG1
631
GGGCAGCGCCTATGCCAACCGCACGGCCCTCTTCCCGGACCTGCT
nGlySerAlaTyrAlaAsnArgThrAlaLeuPheProAspLeuLe
676
GGCACAAGGCAATGCATCCCTGAGGCTGCAGCGCGTGCGTGTGGC
uAlaGlnGlyAsnAlaSerLeuArgLeuGlnArgValArgValAl
721
GGACGAGGGCAGCTTCACCTGCTTCGTGAGCATCCGGGATTTCCGG
aAspGluGlyS rPheThrCysPheValSerIleArgAspPheG1

Fig. 2

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766 CAGCGCTGCCGTCAGCCTGCAGGTGGCCGCTCCCTACTCGAAGCC
ySerAlaAlaValSerLeuGlnValAlaAlaProTyrSerLysPr
811 CAGCATGACCCTGGAGCCCAACAAGGACCTGCGGCCAGGGGACAC
oSerMetThrLeuGluProAsnLysAspLeuArgProGlyAspTh
856 GGTGACCATCACGTGCTCCAGCTACCGGGGCTACCCTGAGGCTGA
rValThrIleThrCysSerSerTyrArgGlyTyrProGluAlaGl
901 GGTGTTCTGGCAGGATGGGCAGGGTGTGCCCCTGACTGGCAACGT
uValPheTrpGlnAspGlyGlnGlyValProLeuThrGlyAsnVa
946 GACCACGTCGCAGATGGCCAACGAGCAGGGCTTGTTTGATGTGCA
lThrThrSerGlnMetAlaAsnGluGlnGlyLeuPheAspValHi
991 CAGCGTCCTGCGGGTGGTGCTGGGTGCGAATGGCACCTACAGCTG
sSerValLeuArgValValLeuGlyAlaAsnGlyThrTyrSerCy
1036 CCTGGTGCGCAACCCCGTGCTGCAGCAGGATGCGCACGGCTCTGT
sLeuValArgAsnProValLeuGlnGlnAspAlaHisGlySerVa
1081 CACCATCACAGGGCAGCCTATGACATTCCCCCAGAGGCCCTGTG
lThrIleThrGlyGlnProMetThrPheProProGluAlaLeuTr
1126 GGTGACCGTGGGGCTCTCTGTCTGTCTCATTGCACTGCTGGTGGC
pValThrValGlyLeuSerValCysLeuIleAlaLeuLeuValAl
1171 CCTGGCTTTCGTGTGCTGGAGAAAGATCAAACAGAGCTGTGAGGA
aLeuAlaPheValCysTrpArgLysIleLysGlnSerCysGluGl
1216 GGAGAATGCAGGAGCCGAGGACCAGGATGGGGAGGGAGAAGGCTC
uGluAsnAlaGlyAlaGluAspGlnAspGlyGluGlyGluGlySe
1261 CAAGACAGCCCTGCAGCCTCTGAAACACTCTGACAGCAAAGAAGA
rLysThrAlaLeuGlnProLeuLysHisSerAspSerLysGluAs
1306 TGATGGACAAGAAATAGCCTGACCATGAGGACCAGGGAGCTGCTA
pAspGlyGlnGluIleAla
1351 CCCCTCCCTACAGCTCCTACCCCTCTGGCTGCAATGGGGCTGCACT
1396 GTGAGCCCTGCCCCCAACAGATGCATCCTGCTCTGACAGGTGGGC
1441 TCCTTCTCCAAAGGATGCGATACACAGACCACTGTGCAGCCTTAT
1486 TTCTCCAATGGACATGATTCCCAAGTCATCCTGCTGCCTTTTTTC
1531 TTATAGACACAATGAACAGACCACCCACAACCTTAGTTCTCTAAG
1576 TCATCCTGCCTGCTGCCTTATTTACAGTACATACATTTCTTAGG
1621 GACACAGTACACTGACCACATCACCACCCTCTTCTTCCAGTGCTG
1666 CGTGGACCATCTGGCTGCCTTTTTTCTCCAAAAGATGCAATATTC

Fig. 2 Continued

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1711 AGACTGACTGACCCCCTGCCTTATTTACCAAAGACACGATGCAT
1756 AGTCACCCCGGCCTTGTTTCTCCAATGGCCGTGATACACTAGTGA
1801 TCATGTTTACGCCCTGCTTCCACCTGCATAGAATCTTTTCTTCTCA
1846 GACAGGGACAGTGCGGCCTCAACATCTCCTGGAGTCTAGAAGCTG
1891 TTTCTTTTCCCCCTCCTTCCTCCTCTTGCTCTAGCCTTAATACTGG
1936 CCTTTTCCCTCCCTGCCCCAAGTGAAGACAGGGCACTCTGCGCCC
1981 ACCACATGCACAGCTGTGCATGGAGACCTGCAGGTGCACGTGCTG
2026 GAACACGTGTGGTTCCCCCCTGGCCCAGCCTCCTCTGCAGTGCCC
2071 CTCTCCCCCTGCCCATCCTCCCCACGGAAGCATGTGCTGGTCACAC
2116 TGGTTCTCCAGGGGTCTGTGATGGGGCCCCCTGGGGGTCAGCTTCT
2161 GTCCCTCTGCCTTCTCACCTCTTTGTTCTTTCTTTTCATGTATC
2206 CATTGAGTTGATGTTTATTGAGCAACTACAGATGTCAGCACTGTG
2251 TTAGGTGCTGGGGGCCCTGCGTGGGAAGATAAAGTTCTTCCCTCA
2296 AGGACTCCCCATCCAGCTGGGAGACAGACAACCTAACTACACTGCA
2341 CCCTGCGGTTTGCAGGGGGCTCCTGCCTGGCTCCCTGCTCCACAC
2386 CTCTCTGTGGCTCAAGGCTTCTGATACCTCACCCCCATCCCA
2431 CCCATAATTCTTACCCAGAGCATGGGGTTGGGGCGGAAACCTGGA
2476 GAGAGGGACATAGCCCCCTGCCACGGCTAGAGAATCTGGTGGTGT
2521 CCAAAATGTCTGTCCAGGTGTGGGCAGGTGGGCAGGCACCAAGGC
2566 CCTCTGGACCTTTTCATAGCAGCAGAAAAGGCAGAGCCTGGGGCAG
2611 GGCAGGGCCAGGAATGCTTTGGGGACACCGAGGGGACTGCCCCC
2656 ACCCCCACCATGGTGCTATTCTGGGGCTGGGGCAGTCTTTTCTCTG
2701 GCTTGCTCTGGCCAGCTCCCGGCCTCTGGTAGAGTGAGACTTCA
2746 GACGTTCTGATGCCTTCCGGATGTCATCTCTCCCTGCCCCAGGAA
2791 TGGAAGATGTGAGGACTTCTAATTTAAATGTGGGACTCGGAGGGA
2836 TTTTGTAAGTGGGGGTATATTTTGGGGAAAATAAATGTCTTTGT
2881 AAAAA

Fig. 2 Continued

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Translated Protein 534 aa-Frame: 3-Nucleotide 60 to 1661
2/14/00

1
GCGGCCGCGGGGCAGCCTTCCACCACGGGGAGCCCAGCTGTCAGC
46
CGCCTCACAGGAAGATGCTGCGTCGGCGGGGCAGCCCTGGCATGG
MetLeuArgArgArgGlySerProGlyMetG
91
GTGTGCATGTGGGTGCAGCCCTGGGAGCACTGTGGTTCTGCCTCA
lyValHisValGlyAlaAlaLeuGlyAlaLeuTrpPheCysLeuT
136
CAGGAGCCCTGGAGGTCCAGGTCCCTGAAGACCCAGTGGTGGCAC
hrGlyAlaLeuGluValGlnValProGluAspProValValAlaL
181
TGGTGGGCACCGATGCCACCCTGTGCTGCTCCTTCTCCCCTGAGC
euValGlyThrAspAlaThrLeuCysCysSerPheSerProGluP
226
CTGGCTTCAGCCTGGCACAGCTCAACCTCATCTGGCAGCTGACAG
roGlyPheSerLeuAlaGlnLeuAsnLeuIleTrpGlnLeuThra
271
ATACCAAACAGCTGGTGCACAGCTTTGCTGAGGGCCAGGACCAGG
spThrLysGlnLeuValHisSerPheAlaGluGlyGlnAspGlnG
316
GCAGCGCCTATGCCAACCGCACGGCCCTCTTCCCGGACCTGCTGG
lySerAlaTyrAlaAsnArgThrAlaLeuPheProAspLeuLeuA
361
CACAGGGCAACGCATCCCTGAGGCTGCAGCGCGTGCCTGTGGCGG
laGlnGlyAsnAlaSerLeuArgLeuGlnArgValArgValAlaA
406
ACGAGGGCAGCTTCACCTGCTTCGTGAGCATCCGGGATTTCCGGCA
spGluGlySerPheThrCysPheValSerIleArgAspPheGlyS
451
GCGCTGCCGTCAGCCTGCAGGTGGCCGCTCCCTACTCGAAGCCCA
erAlaAlaValSerLeuGlnValAlaAlaProTyrSerLysProS
496
GCATGACCCTGGAGCCCAACAAGGACCTGCGGCCAGGGGACACGG
erMetThrLeuGluProAsnLysAspLeuArgProGlyAspThrV
541
TGACCATCACGTGCTCCAGCTACCAGGGCTACCCTGAGGCTGAGG
alThrIleThrCysSerSerTyrGlnGlyTyrProGluAlaGluV
586
TGTTCTGGCAGGATGGGCAGGGTGTGCCCTGACTGGCAACGTGA
alPheTrpGlnAspGlyGlnGlyValProLeuThrGlyAsnValT
631
CCACGTCGCAGATGGCCAACGAGCAGGGCTTGTGTTGATGTGCACA
hrThrSerGlnMetAlaAsnGluGlnGlyLeuPheAspValHisS
676
GCATCCTGCGGGTGGTGCTGGGTGCAAATGGCACCTACAGCTGCC
erIleLeuArgValValLeuGlyAlaAsnGlyThrTyrSerCysL
721
TGGTGGCAACCCCGTGCTGCAGCAGGATGCGCACAGCTCTGTCA
euValArgAsnProValLeuGlnGlnAspAlaHisSerSerValT

Fig. 3

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766 CCATCACACCCCAGAGAAGCCCCACAGGAGCCGTGGAGGTCCAGG
hrIleThrProGlnArgSerProThrGlyAlaValGluValGlnV
811 TCCCTGAGGACCCGGTGGTGGCCCTAGTGGGCACCGATGCCACCC
alProGluAspProValValAlaLeuValGlyThrAspAlaThrL
856 TGGCTGCTCCTTCTCCCCGAGCCTGGCTTCAGCCTGGCACAGC
euArgCysSerPheSerProGluProGlyPheSerLeuAlaGlnL
901 TCAACCTCATCTGGCAGCTGACAGACACCAAACAGCTGGTGCACA
euAsnLeuIleTrpGlnLeuThrAspThrLysGlnLeuValHisS
946 GTTTCACCGAAGGCCGGGACCAGGGCAGCGCCTATGCCAACCGCA
erPheThrGluGlyArgAspGlnGlySerAlaTyrAlaAsnArgT
991 CGGCCCTCTTCCCGGACCTGCTGGCACAAAGGCAATGCATCCCTGA
hrAlaLeuPheProAspLeuLeuAlaGlnGlyAsnAlaSerLeuA
1036 GGCTGCAGCGCGTGCCTGTGGCGGACGAGGGCAGCTTCACCTGCT
rgLeuGlnArgValArgValAlaAspGluGlySerPheThrCysP
1081 TCGTGAGCATCCGGGATTTCCGGCAGCGCTGCCGTCAGCCTGCAGG
heValSerIleArgAspPheGlySerAlaAlaValSerLeuGlnV
1126 TGGCCGCTCCCTACTCGAAGCCCAGCATGACCCTGGAGCCCCACA
alAlaAlaProTyrSerLysProSerMetThrLeuGluProAsnL
1171 AGGACCTGCGGCCAGGGGACACGGTGACCATCACGTGCTCCAGCT
ysAspLeuArgProGlyAspThrValThrIleThrCysSerSerT
1216 ACCGGGGCTACCCTGAGGCTGAGGTGTTCTGGCAGGATGGGCAGG
yrArgGlyTyrProGluAlaGluValPheTrpGlnAspGlyGlnG
1261 GTGTGCCCCCTGACTGGCAACGTGACCACGTCGCAGATGGCCAACG
lyValProLeuThrGlyAsnValThrThrSerGlnMetAlaAsnG
1306 AGCAGGGCTTGTTTGATGTGCACAGCGTCCTGCGGGTGGTGCTGG
luGlnGlyLeuPheAspValHisSerValLeuArgValValLeuG
1351 GTGCGAATGGCACCTACAGCTGCCTGGTGGCGCAACCCCGTGCTGC
lyAlaAsnGlyThrTyrSerCysLeuValArgAsnProValLeuG
1396 AGCAGGATGCGCACGGCTCTGTCAACCATCACAGGGCAGCCTATGA
lnGlnAspAlaHisGlySerValThrIleThrGlyGlnProMetT
1441 CATTCCCCCAGAGGCCCTGTGGGTGACCGTGGGGCTGTCTGTCT
hrPheProProGluAlaLeuTrpValThrValGlyLeuSerValC
1486 GTCTCATTGCACTGCTGGTGGCCCTGGCTTTCGTGTGCTGGAGAA
ysLeuIleAlaLeuLeuValAlaLeuAlaPheValCysTrpArgL
1531 AGATCAAACAGAGCTGTGAGGAGGAGAATGCAGGAGCTGAGGACC
ysIleLysGlnSerCysGluGluGluAsnAlaGlyAlaGluAspG
1576 AGGATGGGGAGGGAGAAGGCTCCAAGACAGCCCTGCAGCCTCTGA
lnAspGlyGluGlyGluGlySerLysThrAlaLeuGlnProLeuL

Fig. 3 Continued

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1621 AACACTCTGACAGCAAAGAAGATGATGGACAAGAAATAGCCTGAC
ysHisSerAspSerLysGluAspAspGlyGlnGluIleAla
1666 CATGAGGACCAGGGAGCTGCTACCCCTCCCTACAGCTCCTACCCCT
1711 CTGGCTGCAATGGGGCTGCACTGTGAGCCCTGCCCCAACAGATG
1756 CATCCTGCTCTGACAGGTGGGCTCCTTCTCCAAAGGATGCGATAC
1801 ACAGACCACTGTGCAGCCTTATTTCTCCAATGGACATGATTCCCA
1846 AGTCATCCTGCTGCCTTTTTTCTTATAGACACAATGAACAGACCA
1891 CCCACAACCTTAGTTCTCTAAGTCATCCTGCCTGCTGCCTTATTT
1936 CACAGTACATACATTTCTTAGGGACACAGTACACTGACCACATCA
1981 CCACCCTCTTCTTCCAGTGCTGCGTGGACCATCTGGCTGCCTTTT
2026 TTCTCCAAAAGATGCAATATTCAGACTGACTGACCCCTGCCTTA
2071 TTTCACCAAAGACACGATGCATAGTCACCCCGACCTTGTTTCTCC
2116 AATGGCCGTGATACACTAGTGATCATGTTTCAGCCCTGCTTCCACC
2161 TGCATAGAATCTTTTCTTCTCAGACAGGGACAGTGCGGCCTCAAC
2206 ATCTCCTGGAGTCTAGGCGGCCGC

Fig. 3 Continued

WO 01/18204

PCT/US00/24220

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Multible Alignment:

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B7-1 HUMAN      --MGHTRRQGTSPSPCPYLNFPOHVLAGE--HFCSGVIEVTKKREVAITPSCGHNVSV
Q28499_rhesus_B7-1 --MGHTRRQETISPSPCPYLKFOHVLAGE--HFCSGVIEVTKKREVAITPSCGHNVSV
B7-1 RABBIT     --MGHTLRPGTLPFLCLHLKLCVHVLAGE--HFSSGTSQVTKSVREVAITPSCGHNVSI
U57755_cat_B7-1 --MGHAAKWKTPLLKHPYPKLPFHHVLAGE--YFCSEIDVTKVREVAITPSCGHNVSI
B7_1 MOUSE     MACNCQLMQDTPLIAFPFCLRLIIFVALLRLSOVSSDVDEQLSKSVTKVLPGERANSFH
AF157827_cat_B7-2 -----MGICDSTMGSETHVMAI-----LSGVSSKSKQVFNKIGELPGPEITNSQ
aaf17297_dog_B7-2 -----MYLICTMSENNHFFVNI-----LYGAASKSKQVFNKIGELPGPEITNSQ
176088_pig_B7-2 -----MGISNHFVMAI-----LYGAASKSKQVFNKIGELPGPEITNSQ
u04343_hu_B7-2 -----MGISNHFVMAI-----LYGAASKSKQVFNKIGELPGPEITNSQ
P42082_mus_B7-2 -----MDPCTMGFAILFFVTVI-----LSDAVSVETQVFNNGVLPPEPTKAQ
aac52336_mus_B7-2_alt.spl -----MGFAILFFVTVI-----LSDAVSVETQVFNNGVLPPEPTKAQ
mz5020.protein    -----MLRRRGSPGMGVHGAALGNWFCITGALEVQVPEDHVALVGTDAFLCCSSPEP
Q99420q99420_put_hum_B7-3 ----MASFLAFLLLNFRCLILQLIAPHSAQFSVLGPSGHILAVGCDLPECHLFPDM
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B7-1 HUMAN      E-EIAQTRDVKOKENAVLTMS--GDMN--LWPEYKRTDIEDITNN--LSIVILAI
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B7-1 RABBIT     D-EIARTRDVKORDQAVLSIS--GQVE--LWPEYKRTDIEDITNN--LSIVILAI
U57755_cat_B7-1 K-EIIEIRLVKOKDEAVLAVES--GKVQ--LWPEYKRTDIEDITNN--LSIVILAI
B7_1 MOUSE     E-DESEDRDVKOKENAVLSVIA--GALK--LWPEYKRTDIEDITNN--LSIVILAI
AF157827_cat_B7-2 NISLDELVVFODQDAVLYEYLR--GKNPQNVHLKTKGRTSEDKIN--LPERLHNV
aaf17297_dog_B7-2 NISLDELVVFODQDAVLYEYLR--GKNPQNVHLKTKGRTSEDKIN--LPERLHNV
176088_pig_B7-2 NISLDELVVFODQDAVLYEYLR--GKPKPNVNSVYMGRTSEDOAT--LPERLHNV
u04343_hu_B7-2 NISLSELVVFODQDAVLYEYLR--GKPKFDSVHSVYMGRTSEDSDS--LPERLHNV
P42082_mus_B7-2 NISLSELVVFODQDAVLYEYLR--GKPKLDSVNAVYMGRTSEDRNN--LPERLHNV
aac52336_mus_B7-2_alt.spl NISLSELVVFODQDAVLYEYLR--GKPKLDSVNAVYMGRTSEDRNN--LPERLHNV
mz5020.protein    GFSLAQNLNLTQLTIRQLVHSEVAGQDQ--GSANVNRITALEPDLAQGNASLRLRV
Q99420q99420_put_hum_B7-3 S--AETHELVVSSSLRQVNVYADGREVEDRQSAPVYGRITSILRDGITAGKAAFRUHV
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B7-1 HUMAN      RPSDEGAYCGVILKVKDIFKRELAEVLSVRADPTPSIEDSEIIPPSN--LRRTICS
Q28499_rhesus_B7-1 RPSDEGAYCGVILKVKDIFKRELAEVLSVRADPTPSIEDSEIIPPSN--LRRTICS
B7-1 RABBIT     RPSDYGAYAGVIOKNGSFRRELTSAVLSIRADFPVDDIADIGHPDEN--VKRRIGCS
U57755_cat_B7-1 RPSDNGVAGVIOKNGSFRRELTSAVLSIRADFPVDDIADIGHPDEN--VKRRIGCS
B7_1 MOUSE     VPSDYGAYCGVILKVKDIFKRELAEVLSVRADPTPSIEDSEIIPPSN--LRRTICS
AF157827_cat_B7-2 QKNDGAYCGVILKVKDIFKRELAEVLSVRADPTPSIEDSEIIPPSN--LRRTICS
aaf17297_dog_B7-2 QKNDGAYCGVILKVKDIFKRELAEVLSVRADPTPSIEDSEIIPPSN--LRRTICS
176088_pig_B7-2 QKNDGAYCGVILKVKDIFKRELAEVLSVRADPTPSIEDSEIIPPSN--LRRTICS
u04343_hu_B7-2 QKNDGAYCGVILKVKDIFKRELAEVLSVRADPTPSIEDSEIIPPSN--LRRTICS
P42082_mus_B7-2 QKNDGAYCGVILKVKDIFKRELAEVLSVRADPTPSIEDSEIIPPSN--LRRTICS
aac52336_mus_B7-2_alt.spl QKNDGAYCGVILKVKDIFKRELAEVLSVRADPTPSIEDSEIIPPSN--LRRTICS
mz5020.protein    RNDGEGAYCGVILKVKDIFKRELAEVLSVRADPTPSIEDSEIIPPSN--LRRTICS
Q99420q99420_put_hum_B7-3 TGSDEWYLGAFQDGFY----EKAIVGKVAALGSDLENVWKGKIDGG--LH-LEGR
```

```
B7-1 HUMAN      NSGGPEPILSVLENGE--ELNAINTVS--ODPEELIYAVSSKDDNMTTNH--SPFG
Q28499_rhesus_B7-1 NSGGPEPILSVLENGE--ELNAINTVS--ODPEELIYAVSSKDDNMTTNH--SPFG
B7-1 RABBIT     ASGGPEPILSVLENGE--ELNAINTVS--ODPEELIYAVSSKDDNMTTNH--SPFG
U57755_cat_B7-1 NSGGPEPILSVLENGE--ELNAINTVS--ODPEELIYAVSSKDDNMTTNH--SPFG
B7_1 MOUSE     ASGGPEPILSVLENGE--ELNAINTVS--ODPEELIYAVSSKDDNMTTNH--SPFG
AF157827_cat_B7-2 SIQGVPEPILSVLENGE--ELNAINTVS--ODPEELIYAVSSKDDNMTTNH--SPFG
aaf17297_dog_B7-2 SIQGVPEPILSVLENGE--ELNAINTVS--ODPEELIYAVSSKDDNMTTNH--SPFG
176088_pig_B7-2 SIQGVPEPILSVLENGE--ELNAINTVS--ODPEELIYAVSSKDDNMTTNH--SPFG
u04343_hu_B7-2 SIQGVPEPILSVLENGE--ELNAINTVS--ODPEELIYAVSSKDDNMTTNH--SPFG
P42082_mus_B7-2 SIQGVPEPILSVLENGE--ELNAINTVS--ODPEELIYAVSSKDDNMTTNH--SPFG
aac52336_mus_B7-2_alt.spl SIQGVPEPILSVLENGE--ELNAINTVS--ODPEELIYAVSSKDDNMTTNH--SPFG
mz5020.protein    SIQGVPEPILSVLENGE--ELNAINTVS--ODPEELIYAVSSKDDNMTTNH--SPFG
Q99420q99420_put_hum_B7-3 SIQGVPEPILSVLENGE--ELNAINTVS--ODPEELIYAVSSKDDNMTTNH--SPFG
```

Fig. 4

PCT/US00/24220

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LNYGEPYNN--QT--ENNTTKQE-----HFDDN--LLPSNAITLIS-----VAGEVY
LNYGEPYNN--QT--ENNTTKQE-----HFDDN--LLPSNAITLIS-----VAGEVY
LNYGEPNYS--QI--EPNKKPKQ-----EPDID--QLPFIQILIPVSG-AL--VETAVY
LNYGEPNYS--QI--ENYKKEP-----QPSNN--QLWIIILSSVSGVIG--VETAVY
LNYGDAYS--ED--EYKKEPPE-----DFPDS--KNTLVIFGAGFG--A--VETAVY
AKNLEPDKLL--SLPNDIAQPKD-----KDEQ--KHVILDAALIV--MF--VYCCGV
VIOLESPKP--SLPNDIAHTKP-----TDG--DHIIIDALIV--ML--VILCGV
VIOLESPKLLF--SLPNDIAKPPV-----QFVP--DHIIIDALIV--TV--VYCCGV
HETDKTLL--SPSIELEDQ-----PPP--DHIPNITVLP--TV--LLVAF
VLETESKTS--SKPLNTQEFPS-----QTYKEITAS--VT--VALTAV
VLETESKTS--SKPLNTQEFPS-----QTYKEITAS--VT--VALTAV
LVNIPVFOODAE--SVTITPQRSPTGAVEVQV--EDFVVALVGLDITRCSFSPEPGFSIAQ
TQNSLGLAEK--HASTIARPPFR-----SAQRHDAIAG--TLFVILITLGA

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COLTYCFAPFC-----REKRN-----RLRFSVRPV-----
COLTYCFAPFC-----REKRN-----RLRFSVRPV-----
YCLACREVAFW-----KRTKRN-----YVGTLELSP-----YLGAQSSG-----
RCLVHRPAFW-----RQREMGRA-----RKWRSHLST-----
VVLKRCFCF-----SCFRNEA-----BRETNLSLF-----GPEEALAEQTVFL-----
SFKTLRKRF-----QPGSHC-----EHLRFRKEK-----QTNRVVPYHVPERSD-----
FFTLRKRF-----QPGSHC-----EHLRFRKEK-----QTNRVVPYHVPERSD-----
SFMTLRKRF-----QPGSHCG-----EHLRFRKEK-----QTKNRAEVHE--RSD-----
CLLTKWRF-----RPRNSYK-----GNTFRKEK-----QTKKREKIHIPERSD-----
LLLTVCHRPN-----QPSFPSNT-----ASFLRDSN-----ADRETINL-----KE-----
LLLTVCHRPN-----QPSFPSNT-----ASFLRDSN-----ADRETINL-----KE-----
LALTLQTLTL-----QLVSTTEGRDQGSAYANLTFPDLAQGNASRLQVRVADG-----
GYFLWOOOEKTKTKRKREOELEMAWSTMKOEKTRVKLLEELRWRSIOYASGRER-----

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[illegible]

QDGGGVPLTGNNVTTSQMANEQGLFDVHSVLRRVLCANGTYSCLVRNPVLOQDAEGSVTTIT

SUBSTITUTE SHEET (RULE 26)

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B7-1_HUMAN	-----
Q28499_rhesus_B7-1	-----
B7-1_RABBIT	-----
U57755_cat_B7_1	-----
B7-1_MOUSE	-----
AF157827_cat_B7-2	-----
aaf17297_dog_B7-2	-----
176088-pig_B7-2	-----
u04343_hu_B7-2	-----
P42082_mus_B7_2	-----
aac52336_mus_B7-2_alt.spl	-----
mz5020.protein	GQPMTFPPPEALWVTVGLSVCLIALLLVALAFVCWRKIKQSCEENAGAEDQDGEGEKSKTA
Q99420q99420_put_hum_B7-3	-----
B7-1_HUMAN	-----
Q28499_rhesus_B7-1	-----
B7-1_RABBIT	-----
U57755_cat_B7_1	-----
B7-1_MOUSE	-----
AF157827_cat_B7-2	-----
aaf17297_dog_B7-2	-----
176088-pig_B7-2	-----
u04343_hu_B7-2	-----
P42082_mus_B7_2	-----
aac52336_mus_B7-2_alt.spl	-----
mz5020.protein	LQPLKHSDSKEDDGQETL
Q99420q99420_put_hum_B7-3	-----

Fig. 4 Continued

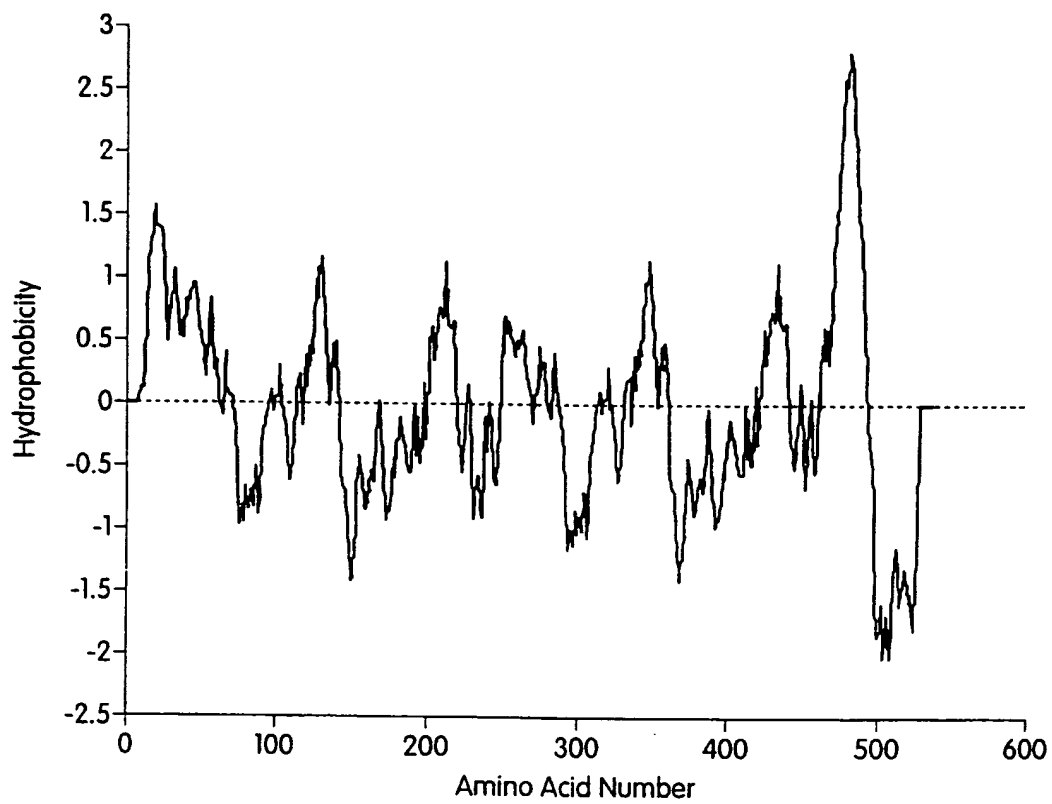


Fig. 5